

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 10/516,558A
Source: PT
Date Processed by STIC: 3/9/06

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1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
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Revised 01/10/06



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt
 Output Set: N:\CRF4\03092006\J516558A.raw

3 <110> APPLICANT: Chano, Tokuhiro
 4 Okabe, Hidetoshi
 5 Ikegawa, Shiro
 7 <120> TITLE OF INVENTION: RB1 gene induced protein (RB1CC1) and gene
 9 <130> FILE REFERENCE: 3190-070
 11 <140> CURRENT APPLICATION NUMBER: US 10/516,558A
 12 <141> CURRENT FILING DATE: 2004-11-30
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00882
 15 <151> PRIOR FILING DATE: 2003-01-30
 17 <150> PRIOR APPLICATION NUMBER: JP P2002-161400
 18 <151> PRIOR FILING DATE: 2002-06-03
 20 <150> PRIOR APPLICATION NUMBER: JP P2002-214978
 21 <151> PRIOR FILING DATE: 2002-07-24
 23 <160> NUMBER OF SEQ ID NOS: 132
 25 <170> SOFTWARE: PatentIn version 3.1

Jan 1-16, 18

ERRORED SEQUENCES

27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1594
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Unknown
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: human RB1CC1
 35 <400> SEQUENCE: 1
 37 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
 38 1 5 10 15
 41 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
 42 20 25 30
 45 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
 46 35 40 45
 49 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
 50 50 55 60
 53 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
 54 65 70 75 80
 E--> 57
 58 Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn
 E--> 59 85 90 95
 62 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
 E--> 63 100 105 110
 66 His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val
 E--> 67 115 120 125

Does Not Comply
 Corrected Diskette Needed

delete
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 error)

Per 1.824 of

Sequence Rules,

no page numbers allowed

3/9/2006 computer
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Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

70 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
 E--> 71 130 135 140
 74 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
 E--> 75 145 150 155 160
 78 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
 E--> 79 165 170 175
 82 Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
 E--> 83 180 185 190
 86 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
 E--> 87 195 200 205
 90 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro
 E--> 91 210 215 220
 94 Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu
 E--> 95 225 230 235 240
 98 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Glu Ser Leu Leu Thr
 E--> 99 245 250 255
 102 Ser Phe Pro Lys Ser Val Glu His Val Ser Pro Asp Thr Ala Asp Ala
 E--> 103 260 265 270
 106 Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln
 E--> 107 275 280 285
 110 Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe
 E--> 111 290 295 300
 E--> 114
 116 Asn Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp
 E--> 117 305 310 315 320
 120 Val Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp
 E--> 121 325 330 335
 124 Pro Arg Ile Ile Arg Pro Phe Ile Ala Glu Cys Arg Gln Thr Ile Ala
 E--> 125 340 345 350
 128 Lys Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg
 E--> 129 355 360 365
 132 Leu Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Gly Arg Leu Val Asn
 E--> 133 370 375 380
 136 Glu Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Lys Arg Ala
 E--> 137 385 390 395 400
 140 Glu Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His
 E--> 141 405 410 415
 144 Ala Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp
 E--> 145 420 425 430
 148 Ile Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu
 E--> 149 435 440 445
 152 His Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln
 E--> 153 450 455 460
 156 Asp Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu
 E--> 157 465 470 475 480
 160 Glu Arg Val Lys Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr
 E--> 161 485 490 495
 164 Cys Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His
 E--> 165 500 505 510

-2- *Delete* ↗

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Input Set : A:\3190-070 Sequence Listing.txt

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168	Tyr Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Arg Leu Tyr			
E--> 169	515	520	525	
E--> 171			-3-	
173	Glu Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys			
E--> 174	530	535	540	
177	Ser Phe Leu Arg Asn Arg Leu Phe Arg Gly Leu Asp Ser Trp Pro Pro			
E--> 178	545	550	555	560
181	Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp			
E--> 182	565	570	575	
185	Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu			
E--> 186	580	585	590	
189	Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu			
E--> 190	595	600	605	
193	His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser			
E--> 194	610	615	620	
197	Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys			
E--> 198	625	630	635	640
201	Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met			
E--> 202	645	650	655	
205	Glu Ser Thr Ala Gly Ile Thr Thr Thr Ser Pro Arg Thr Pro Pro			
E--> 206	660	665	670	
209	Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu			
E--> 210	675	680	685	
213	Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr			
E--> 214	690	695	700	
217	Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp			
E--> 218	705	710	715	720
221	Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val			
E--> 222	725	730	735	
225	Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser			
E--> 226	740	745	750	
E--> 228			-4-	
229	Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val			
E--> 230	755	760	765	
233	Ile Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Asn Val Cys Gly			
E--> 234	770	775	780	
237	Lys Glu Asp Phe Gly Asp His Thr Ser Leu Asn Val Gln Leu Glu Arg			
E--> 238	785	790	795	800
241	Cys Arg Val Val Ala Gln Asp Ser His Phe Ser Ile Gln Thr Ile Lys			
E--> 242	805	810	815	
245	Glu Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp			
E--> 246	820	825	830	
249	Phe Ser Asn Ser Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile			
E--> 250	835	840	845	
253	Glu Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln			
E--> 254	850	855	860	
257	Lys Glu Leu Leu Ser Leu Lys Asn Glu Tyr Glu Gly Lys Leu Asp Gly			
E--> 258	865	870	875	880
261	Leu Ile Lys Glu Thr Glu Glu Asn Glu Asn Lys Ile Lys Lys Leu Lys			

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Output Set: N:\CRF4\03092006\J516558A.raw

E--> 262	885	890	895
265	Gly Glu Leu Val Cys Leu Glu Glu Val Leu Gln Asn Lys Asp Asn Glu		
E--> 266	900	905	910
269	Phe Ala Leu Val Lys His Glu Lys Glu Ala Val Ile Cys Leu Gln Asn		
E--> 270	915	920	925
273	Glu Lys Asp Gln Lys Leu Leu Glu Met Glu Asn Ile Met His Ser Gln		
E--> 274	930	935	940
277	Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile Val Leu Glu		
E--> 278	945	950	955
281	Asp Leu Lys Lys Leu His Val Glu Asn Asp Glu Lys Leu Gln Leu Leu		
E--> 282	965	970	975
E--> 286		-5-	
287	Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys Glu Leu Glu		
E--> 288	980	985	990
291	Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys Val Met Thr		
E--> 292	995	1000	1005
295	Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn Gln Gln		
E--> 296	1010	1015	1020
299	Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln Glu		
E--> 300	1025	1030	1035
303	Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu		
E--> 304	1040	1045	1050
307	Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu		
E--> 308	1055	1060	1065
311	Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Ser Arg Ala		
E--> 312	1070	1075	1080
315	Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu		
E--> 316	1085	1090	1095
319	Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp		
E--> 320	1100	1105	1110
323	Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu		
E--> 324	1115	1120	1125
327	Met Thr Ile Glu Lys Asp Gln Arg Ile Ser Glu Leu Ile Ser Arg		
E--> 328	1130	1135	1140
331	His Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Val		
E--> 332	1145	1150	1155
335	Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Asn Leu Lys		
E--> 336	1160	1165	1170
339	Glu Gln Ile Ile Glu Leu Gln Ser Lys Leu Asp Ser Glu Leu Ser		
E--> 340	1175	1180	1185
E--> 343		-6-	
344	Ala Leu Glu Arg Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu		
E--> 345	1190	1195	1200
348	Lys Tyr Glu Ala Ile Ile Gln Asn Leu Glu Lys Asp Arg Gln Lys		
E--> 349	1205	1210	1215
352	Leu Val Ser Ser Gln Glu Gln Asp Arg Glu Gln Leu Ile Gln Lys		
E--> 353	1220	1225	1230
356	Leu Asn Cys Glu Lys Asp Glu Ala Ile Gln Thr Ala Leu Lys Glu		
E--> 357	1235	1240	1245

same
error

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Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

459 <210> SEQ ID NO: 2
 460 <211> LENGTH: 1588
 461 <212> TYPE: PRT
 462 <213> ORGANISM: Unknown
 464 <220> FEATURE:
 465 <223> OTHER INFORMATION: mouse Rb1cc1
 467 <400> SEQUENCE: 2

469 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
 470 1 5 10 15
 473 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
 474 20 25 30
 477 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
 478 35 40 45
 481 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
 482 50 55 60
 485 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
 486 65 70 75 80
 489 Cys Asp Arg Ala Pro Ala Ile Pro Lys Ala Thr Phe Ser Thr Glu Asn
 490 85 90 95
 493 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
 494 100 105 110
 497 His Thr Val Ala Ser Arg Thr Gln Leu Ala Val Glu Met Tyr Asp Val
 498 115 120 125
 501 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
 502 130 135 140
 505 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
 506 145 150 155 160
 509 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
 510 165 170 175
 513 Asp Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
 514 180 185 190
 E--> 515 -9- *delete*
 516 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
 E--> 517 195 200 205
 520 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Pro Asp Ser Leu Asn
 E--> 521 210 215 220
 524 Glu His Glu Gly Ser Glu Lys Ala Glu Met Lys Arg Ser Thr Glu Leu
 E--> 525 225 230 235 240
 528 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Thr Ser Leu Val Thr
 E--> 529 245 250 255
 532 Ser Phe His Lys Ser Met Glu His Val Ala Pro Asp Pro Thr Gly Thr
 E--> 533 260 265 270
 536 Glu Arg Gly Lys Glu Leu Arg Glu Ser Cys Gln Ser Thr Val Gln Gln
 E--> 537 275 280 285
 540 Glu Glu Ala Ser Val Asp Ala Lys Asp Ser Asp Leu Pro Phe Phe Asn
 E--> 541 290 295 300
 544 Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp Val
 E--> 545 305 310 315 320
 548 Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp Pro

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647 Ser His Pro Asn Thr Glu Gln Pro Val His Gln Ala Ser Ile Asp Leu
 E--> 648 705 710 715 720
 651 Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val Asn
 E--> 652 725 730 735
 655 Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser Asp
 E--> 656 740 745 750
 660 Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val Ile
 E--> 661 755 760 765
 664 Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Ser Thr Arg Gly Asn
 E--> 665 770 775 780
 668 Glu Gly Phe Gly Asp Arg Ala Ala Leu His Val Gln Leu Glu Lys Cys
 E--> 669 785 790 795 800
 672 Arg Ala Ala Ala Gln Asp Ser His Thr Ser Ile Gln Thr Ile Lys Asp
 E--> 673 805 810 815
 676 Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp Leu
 E--> 677 820 825 830
 680 Ala Asn Tyr Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile Glu
 E--> 681 835 840 845
 684 Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln Gln
 E--> 685 850 855 860
 E--> 687 -12- *same*
 688 Glu Leu Gln Ser Leu Lys Ile Glu Tyr Glu Cys Lys Leu Asp Ala Leu
 E--> 689 865 870 875 880
 692 Val Lys Asp Ser Glu Glu Asn Val Asn Lys Ile Leu Lys Leu Lys Glu
 E--> 693 885 890 895
 696 Asn Leu Val Ser Leu Glu Glu Ala Leu Gln Asn Lys Asp Asn Glu Phe
 E--> 697 900 905 910
 700 Thr Ser Ile Lys His Glu Lys Asp Ala Ile Val Cys Val Gln Gln Glu
 E--> 701 915 920 925
 705 Lys Asp Gln Lys Leu Leu Glu Met Glu Lys Ile Met His Thr Gln His
 E--> 706 930 935 940
 709 Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Met Ala Leu Glu Asp
 E--> 710 945 950 955 960
 713 Leu Lys Lys Leu His Asp Glu Lys Ile Glu Ser Leu Arg Ala Glu Phe
 E--> 714 965 970 975
 717 Gln Cys Leu Glu Glu Asn His Leu Lys Glu Leu Glu Asp Thr Leu His
 E--> 718 980 985 990
 721 Ile Arg His Thr Gln Glu Phe Glu Lys Val Met Thr Asp His Asn Met
 E--> 722 995 1000 1005
 725 Ser Leu Glu Lys Leu Lys Lys Glu Asn Gln Gln Arg Ile Asp Gln
 E--> 726 1010 1015 1020
 730 Met Leu Glu Ser His Ala Ser Thr Ile Gln Glu Lys Glu Gln Gln
 E--> 731 1025 1030 1035
 734 Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu Ser Asp Met Arg
 E--> 735 1040 1045 1050
 738 Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu Ala Glu Thr Asp
 E--> 739 1055 1060 1065
 742 Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Thr Gln Gln Lys Glu
 E--> 743 1070 1075 1080

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E--> 549 325 330 335
 552 Lys Ile Ile Gln Pro Phe Met Leu Glu Cys His Gln Thr Ile Ala Lys
 E--> 553 340 345 350
 556 Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg Leu
 E--> 557 355 360 365
 560 Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Ser Arg Leu Val Asn Glu
 E--> 561 370 375 380
 564 Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Met Arg Ala Glu
 E--> 565 385 390 395 400
 568 Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His Ala
 E--> 569 405 410 415
 E--> 572 -10-
 573 Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp Ile
 E--> 574 420 425 430
 577 Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu His
 E--> 578 435 440 445
 581 Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln Asp
 E--> 582 450 455 460
 585 Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu Glu
 E--> 586 465 470 475 480
 589 Arg Val Arg Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr Cys
 E--> 590 485 490 495
 593 Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His Tyr
 E--> 594 500 505 510
 597 Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Gln Leu Tyr Glu
 E--> 598 515 520 525
 601 Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys Ser
 E--> 602 530 535 540
 605 Phe Leu Arg Asn Arg Leu Phe Lys Gly Leu Asp Ser Trp Pro Ser Ser
 E--> 606 545 550 555 560
 609 Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp Ile
 E--> 610 565 570 575
 613 Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu Val
 E--> 614 580 585 590
 617 Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu His
 E--> 618 595 600 605
 621 Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser Leu
 E--> 622 610 615 620
 625 Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Asn Glu Gln Lys Val
 E--> 626 625 630 635 640
 E--> 628 -11-
 631 Ser Thr Ser Gln Ala Ser Pro Gln Ser Ala Ala Ser Pro Arg Ile Glu
 E--> 632 645 650 655
 635 Ser Thr Thr Gly Ile Thr Thr Thr Ser Pro Lys Thr Pro Pro Pro
 E--> 636 660 665 670
 639 Leu Thr Val Gln Asp Thr Leu Cys Pro Ala Val Cys Pro Leu Glu Glu
 E--> 640 675 680 685
 643 Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr Ile
 E--> 644 690 695 700

*Same
error*

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360 Phe Lys Leu Glu Arg Glu Val Val Glu Lys Glu Leu Leu Glu Lys
 E--> 361 1250 1255 1260
 364 Val Lys His Leu Glu Asn Gln Ile Ala Lys Ser Pro Ala Ile Asp
 E--> 365 1265 1270 1275
 368 Ser Thr Arg Gly Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu
 E--> 369 1280 1285 1290
 372 Lys Leu Gln Glu Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu
 E--> 373 1295 1300 1305
 376 Gln Glu Lys Arg Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser
 E--> 377 1310 1315 1320
 380 Leu Ile Ala Glu Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg
 E--> 381 1325 1330 1335
 384 Glu Lys Met Arg Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys
 E--> 385 1340 1345 1350
 388 Leu Lys Ser Thr Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile
 E--> 389 1355 1360 1365
 392 Glu Ser Leu Ser Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys
 E--> 393 1370 1375 1380
 396 Lys Leu Glu Glu Glu Val Ser Lys Leu Arg Ser Ser Ser Phe Val
 E--> 397 1385 1390 1395
 E--> 401
 402 Pro Ser Pro Tyr Val Ala Thr Ala Pro Glu Leu Tyr Gly Ala Cys
 E--> 403 1400 1405 1410
 406 Ala Pro Glu Leu Pro Gly Glu Ser Asp Arg Ser Ala Val Glu Thr
 E--> 407 1415 1420 1425
 410 Ala Asp Glu Gly Arg Val Asp Ser Ala Met Glu Thr Ser Met Met
 E--> 411 1430 1435 1440
 414 Ser Val Gln Glu Asn Ile His Met Leu Ser Glu Glu Lys Gln Arg
 E--> 415 1445 1450 1455
 418 Ile Met Leu Leu Glu Arg Thr Leu Gln Leu Lys Glu Glu Glu Asn
 E--> 419 1460 1465 1470
 422 Lys Arg Leu Asn Gln Arg Leu Met Ser Gln Ser Met Ser Ser Val
 E--> 423 1475 1480 1485
 426 Ser Ser Arg His Ser Glu Lys Ile Ala Ile Arg Asp Phe Gln Val
 E--> 427 1490 1495 1500
 430 Gly Asp Leu Val Leu Ile Ile Leu Asp Glu Arg His Asp Asn Tyr
 E--> 431 1505 1510 1515
 434 Val Leu Phe Thr Val Ser Pro Thr Leu Tyr Phe Leu His Ser Glu
 E--> 435 1520 1525 1530
 438 Ser Leu Pro Ala Leu Asp Leu Lys Pro Gly Glu Gly Ala Ser Gly
 E--> 439 1535 1540 1545
 442 Ala Ser Arg Arg Pro Trp Val Leu Gly Lys Val Met Glu Lys Glu
 E--> 443 1550 1555 1560
 446 Tyr Cys Gln Ala Lys Lys Ala Gln Asn Arg Phe Lys Val Pro Leu
 E--> 447 1565 1570 1575
 450 Gly Thr Lys Phe Tyr Arg Val Lys Ala Val Ser Trp Asn Lys Lys
 E--> 451 1580 1585 1590
 454 Val
 E--> 458

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Jane

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Input Set : A:\3190-070 Sequence Listing.txt
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E--> 744

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745 Met Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu Asn Leu Arg Thr
 E--> 746 1085 1090 1095
 749 Glu Ile Ser Lys Leu Asn Gln Lys Ile His Asp Asn Asn Glu Ser
 E--> 750 1100 1105 1110
 753 Tyr Gln Val Gly Leu Ser Glu Leu Arg Ala Leu Met Thr Ile Glu
 E--> 754 1115 1120 1125
 758 Lys Asp Gln Cys Ile Ser Glu Leu Ile Ser Arg His Glu Glu Glu
 E--> 759 1130 1135 1140
 762 Ser Asn Ile Leu Lys Ala Glu Leu Asp Asn Val Thr Ser Leu His
 E--> 763 1145 1150 1155
 766 Arg Gln Ala Tyr Glu Ile Glu Lys Lys Leu Lys Glu Gln Ile Val
 E--> 767 1160 1165 1170
 770 Glu Leu Gln Thr Arg Leu Asn Ser Glu Leu Ser Ala Leu Glu Lys
 E--> 771 1175 1180 1185
 774 Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu Lys Tyr Glu Ala
 E--> 775 1190 1195 1200
 778 Leu Ile Gln Asn Leu Glu Lys Asp Lys Glu Arg Leu Val Lys Asn
 E--> 779 1205 1210 1215
 782 His Glu Gln Asp Lys Glu His Leu Ile Gln Glu Leu Asn Phe Glu
 E--> 783 1220 1225 1230
 786 Lys Asn Lys Ala Val Gln Thr Ala Leu Asp Glu Phe Lys Val Glu
 E--> 787 1235 1240 1245
 790 Arg Glu Leu Val Glu Lys Glu Leu Leu Glu Lys Val Lys His Leu
 E--> 791 1250 1255 1260
 794 Glu Asn Gln Ile Ala Lys Thr Pro Ala Phe Glu Ser Ala Arg Glu
 E--> 795 1265 1270 1275
 798 Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu Lys Leu Gln Glu
 E--> 799 1280 1285 1290

E--> 802

-14-

803 Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu Gln Glu Lys Arg
 E--> 804 1295 1300 1305
 807 Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser Leu Ile Ala Glu
 E--> 808 1310 1315 1320
 811 Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg Glu Lys Met Arg
 E--> 812 1325 1330 1335
 815 Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys Leu Lys Ser Thr
 E--> 816 1340 1345 1350
 819 Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile Glu Ser Leu Ser
 E--> 820 1355 1360 1365
 823 Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys Gln Leu Glu Glu
 E--> 824 1370 1375 1380
 827 Glu Val Ser Lys Leu Arg Thr Ser Ser Phe Leu Ser Ser Ala Pro
 E--> 828 1385 1390 1395
 831 Val Ala Ala Ala Pro Glu Leu Tyr Gly Ala Cys Ala Pro Glu Leu
 E--> 832 1400 1405 1410
 835 Pro Gly Glu Pro Glu Arg Ser Val Met Glu Thr Ala Asp Glu Gly
 E--> 836 1415 1420 1425
 839 Arg Leu Asp Ser Ala Met Glu Thr Ser Met Met Ser Val Gln Glu

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,558A

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Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

E--> 840 1430 1435 1440
 843 Asn Met Leu Ser Glu Glu Lys Gln Arg Ile Met Leu Leu Glu Arg
 E--> 844 1445 1450 1455
 847 Thr Leu Gln Leu Lys Glu Glu Glu Asn Lys Arg Leu Asn Gln Arg
 E--> 848 1460 1465 1470
 851 Leu Met Ser Gln Ser Leu Ser Ser Val Ser Ser Arg His Ser Glu
 E--> 852 1475 1480 1485
 855 Lys Ile Ala Ile Arg Asp Phe Gln Val Gly Asp Leu Val Leu Ile
 E--> 856 1490 1495 1500
 E--> 858 -15- same
 861 Ile Leu Asp Glu Arg His Asp Asn Tyr Val Leu Phe Thr Val Ser
 E--> 862 1505 1510 1515
 865 Pro Thr Leu Tyr Phe Leu His Ser Glu Ser Leu Pro Ala Leu Asp
 E--> 866 1520 1525 1530
 868 Leu Lys Pro Gly Glu Gly Ala Ser Gly Ala Ser Arg Arg Pro Trp
 E--> 869 1535 1540 1545
 871 Val Leu Gly Lys Val Met Glu Lys Glu Tyr Cys Gln Ala Lys Lys
 E--> 872 1550 1555 1560
 875 Ala Gln Asn Arg Phe Lys Val Pro Leu Gly Thr Lys Phe Tyr Arg
 E--> 876 1565 1570 1575
 879 Val Lys Ala Val Ser Trp Asn Lys Lys Val
 E--> 880 1580 1585
 882 <210> SEQ ID NO: 3
 883 <211> LENGTH: 6636
 884 <212> TYPE: DNA
 885 <213> ORGANISM: Unknown
 887 <220> FEATURE:
 888 <223> OTHER INFORMATION: human RB1CC1 gene
 890 <400> SEQUENCE: 3
 891 gtcgacaata acaaaccataag ccgcggcggt gtccggggcc ctggcgagcc ctggcggttg 60
 893 cctcagaatc ccccagtgcg ctggggccct cggctctgac aggccgcggc cttctgtccc 120
 895 ccggccccag acccagagcc gagggggctg ctcgcgtcct tgccgcggcc gacccttccc 180
 897 tgccctctag agttcggggc cgcggcgccc gggcgccccgg gacgcggcggtt gttgtgtcgg 240
 899 cttagcggtg ccgaatgggc ggttggtaac cgctgcgcgag gactaggcgg cggcgaaaga 300
 901 tgggccggg ggtcgctggc tctgctgctg ccgcggcgaa aggaggaggc gttgcgggtt 360
 903 ttctgagttt aaccagtaat gccattcagt tgccaatctc aagcaaagca aacataagcc 420
 905 agtttaatc tacttttaa gaaaagtggt agtcctttc acagtgcctg acgttaactgt 480
 907 atcagagggt gaggtaatcgtt ctcacagaat tcagataat catcatgaag ttatatgtat 540
 909 ttctggtaa cactggaaact actctaacat ttgacactga actttacagtg caaaactgtgg 600
 911 cagaccttaa gcatgccatt caaagcaaatac acaagattgc tattcaacac caggtgctgg 660
 913 tggtaatgg aggagaatgc atggctgcag atcgaaatgt gtgtacctac agtgcgtggga 720
 E--> 915 -16- same
 918 cggatacaaa tccaaatttt ctttttaaca aagaaatgtat cttatgcgt cgtccacctg 780
 920 ctattcctaa aactacctt tcgacagaaaa atgacatgga aataaaatgtt gaagaatctc 840
 922 ttatgtgcc tgcagtttt catactgttg cttcaaggac acagcttgcgat ttggaaatgt 900
 924 atgaagttgc caagaaactt tgttctttt gtgaaggctt tgcacatgtat gaacatctc 960
 926 aacaccaagg ctgggctgca atcatggcca acctggagga ctgttcaat tcataccaaa 1020
 928 agctactttt caagtttggaa agtattttt caaattatct gcagtccata gaagacatca 1080
 930 agttaaaaact tactcattta ggaactgcag tttcagtaat ggccaagatt ccactgttgg 1140

RAW SEQUENCE LISTING

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Input Set : A:\3190-070 Sequence Listing.txt

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932	agtgcctaac	cagacatagt	tacagagaat	gtttgggaag	actggattct	ttacctgaac	1200
934	atgaagactc	agaaaaagct	gagacgaaaa	gatccactga	actggtgctc	tctcctgata	1260
936	tgcctagaac	aactaacgaa	tctttgttaa	cctcatttcc	caagtcagtg	gaacatgtgt	1320
938	ccccagatac	cgcagatgct	gaaagtggca	aagaaattag	ggaatcttgc	caaagtactg	1380
940	ttccatcagca	agatgaaact	acgattgaca	ctaaagatgg	tgatctgccc	ttttttaatg	1440
942	tctctttgtt	agactggata	aatgttcaag	atagacctaa	tgatgtggaa	tctttggtca	1500
944	ggaagtgctt	tgattctatg	acgaggctt	atccaaggat	tattcgacc	tttatacgag	1560
946	aatgccgtca	aactattgcc	aaacttgata	atcagaatat	gaaagccatt	aaaggacttg	1620
948	aagatccgct	ctacgcctg	gaccagatga	ttgcttagctg	tggccgactg	gtgaatgaac	1680
950	agaaagagct	tgctcaggga	tttttagcta	atcagaagag	agctgaaaac	ttaaaggatg	1740
952	catctgtatt	acctgattta	tgcctgagtc	acgcaaatac	gttgcattt	atgttgcata	1800
954	atcatagaaa	actgttagat	attaagcaga	agtgtaccac	tgc当地acaa	gaactagcaa	1860
956	ataacctaca	tgtcagactg	aagtgggttt	gctttgtaat	gcttcatgct	gatcaagatg	1920
958	gagagaagtt	acaagctt	ctccgcctcg	taatagagct	gttagaaaga	gtcaaaattg	1980
960	ttgaagctct	tagtacagtt	cctcagatgt	actgcttagc	ttttgtttag	tttgc当地aa	2040
962	aaaaaatgtt	cataaaacac	tacagggagt	gggctgggtc	tttagtcaaa	gatggaaaga	2100
964	gattatatga	agcagaaaaaa	tcaaaaaggg	aatccttgg	aaaatttatt	aggaagtctt	2160
966	tttaagaaa	tcgtctgtt	aggggactgg	actcctggcc	cccttcctt	tgtactcaaa	2220
968	agcctcgaaa	gtttgactgt	gaacttccag	atatttcatt	aaaagattt	cagttctgc	2280
970	aatcattttg	tccttcggaa	gttcagccat	tcctcagggt	tcccttactt	tgtgactttg	2340
972	aacctctaca	ccagcatgta	cttgccttac	ataatttgg	aaaagcagca	caaagtttgg	2400

E--> 974

-17-

975	ataaaaatgtc	acagaccatt	acagatctac	tgagtgaaca	aaaggcatct	gtgagccaga	2460
977	catccccaca	gtctgcttct	tcaccaagga	tggaaagtac	agcaggaatt	acaactacta	2520
979	cctcaccgag	aactcctcca	ccactgactg	ttcaggatcc	cttatgtcct	gcagttgtc	2580
981	ccttagaaga	attatctcca	gatagtattt	atgcacatac	gttgcatttt	gaaactattc	2640
983	cccatccaaa	catagaacag	actattcacc	aagtttctt	agacttggat	tcattagcag	2700
985	aaagtcttga	atcagatttt	atgtctgt	tgaatgagtt	tgtatagaaa	gaaaatttgt	2760
987	cgtctctaa	tcctataagt	gatccacaaa	gcccagaaat	gatggtgaa	tcactttt	2820
989	catcagttat	caatgcgata	gacagtagac	gaatgcagga	tacaaaatgt	tgtggtaagg	2880
991	aggattttgg	agatcatact	tctctgaatg	tccagttgg	aaagatgtaga	gttgc当地cc	2940
993	aagactctca	cttcagttata	caaaccatta	aggaagacct	ttgccactt	agaacattt	3000
995	tacaaaaga	acagtgtgac	ttctcaatt	cattaaaatg	tacagcagta	gaaataagaa	3060
997	acattattga	aaaagtaaaa	tgttctctgg	aaataacact	aaaagaaaaaa	catcaaaaag	3120
999	aactactgtc	tttaaaaaat	gaatatgaag	gtaaacttga	cggactaata	aggaaaactg	3180
1001	aagagaatga	aaacaaaatt	aaaaaattga	agggagagtt	agtatgcctt	gaggaggtt	3240
1003	tacaaaataa	agataatgaa	tttgctttgg	ttaaacatga	aaaagaagct	gtaatctgcc	3300
1005	tgcaaatga	aaaggatcag	aaatttttttt	agatggaaaa	tataatgcac	tctcaaaatt	3360
1007	gtgaaattaa	agaactgaag	cagtcacgag	aaatagtgtt	agaagactta	aaaaagctcc	3420
1009	atgtgaaaa	tgtatgaaag	ttacagttat	tgagggcaga	acttcagttcc	ttggagcaaa	3480
1011	gtcatctaaa	ggaatttagag	gacacacttc	aggtttaggc	catacaagag	tttgagaagg	3540
1013	ttatgacaga	ccacagagtt	tctttggagg	aattaaaaaa	ggaaaatcaa	caaataatta	3600
1015	atcaaataca	agaatctcat	gctgaaattt	tccagggaaa	agaaaaacag	ttacaggaat	3660
1017	taaaactcaa	gttttctgat	ttgtcagaca	cgagatgca	gttagaggtt	gaacttgcgt	3720
1019	tgaaggaagc	agaaaactgt	gaaataaaaa	ttttgttgg	agaaagcaga	gcccagcaga	3780
1021	aggagacctt	gaaatctt	cttgcacaag	agacagaaaa	tttgagaaca	gaaatttagt	3840
1023	aactcaacca	aaagattcag	gataataatg	aaaattatca	ggtgggctt	gcagagctaa	3900
1025	gaactttaat	gacaatttggaa	aaaagatcagc	gtatttccga	gttaatttgc	agacatgaag	3960
1027	aagaatctaa	tataacttaaa	gctgaattaa	acaaagtaac	atctttgcatt	aaccaagcat	4020

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Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

1029	ttgaaaataga	aaaaaaccta	aaagaacaaa	taatttgaact	gcagagtaaa	ttggatttcag	4080
E--> 1031				-18-	Jane		
1032	aattttagtgc	tcttggaaaga	caaaaagatg	aaaaaattac	ccaaacaagaa	gagaaatacg	4140
1034	aagctattat	ccagaacott	gagaaagaca	gacaaaaatt	ggtcagcagc	caggagcaag	4200
1036	acagagaaca	gttaatttcag	aagcttaatt	gtgaaaaaga	tgaagctatt	cagactgccc	4260
1038	taaaagaatt	taaatttggag	agagaagttg	ttgagaaaaga	gttatttagaa	aaagttaaac	4320
1040	atcttgagaa	tcaaatacgca	aaaagtccctg	ccattgactc	taccagagga	gattcttcaa	4380
1042	gcttagttgc	tgaacttcaa	gaaaagctc	aggaagaaaa	agctaagttt	ctagaacaac	4440
1044	ttgaagagca	agaaaaaaaaga	aagaatgaag	aaatgcaaaa	tgttgcgaca	tctttgattg	4500
1046	cggaaacaaca	gaccaatttt	aacactgttt	taacaagaga	gaaaatgaga	aaagaaaaca	4560
1048	taataaaatgt	tcttagtgc	aagttgaaaa	gtacaatgca	gcaacaagaa	cgggataaaag	4620
1050	atttgataga	gtcactttct	gaagatcgag	ctcggttgc	tgagggaaaag	aaaaagcttg	4680
1052	aagaagaagt	cagtaagttg	cgcaagtagca	gtttttttcc	ttcaccatat	gtagctacag	4740
1054	ccccagaact	ttatggagct	tgtgcacctg	aactccagg	tgaatcagat	agatccgctg	4800
1056	tggaaacagc	agatgaagga	agagtggatt	cagcaatgg	gacaagcattg	atgtctgtac	4860
1058	aagaaaatat	tcatatgtt	tctgaagaaa	aacagccgt	aatgctgtt	gaacgaacat	4920
1060	tgcaattgaa	agaagaagaa	aataaacggt	taaatcaaag	actgtatgtct	cagagcatgt	4980
1062	cttcagtatc	ttcaaggcat	tctgaaaaaa	tagtatttag	agattttcag	gtgggagatt	5040
1064	tggtaactcat	catcctagac	gaacgccatg	acaattatgt	gttattttact	gttagtccta	5100
1066	ctttatattt	tctacattca	gagtctctac	ctggccctgga	tctcaaaacca	ggtgagggtg	5160
1068	cttcaggtgc	atctagaaga	ccctgggtac	ttggaaaagt	aatggaaaaaa	gaataactgtc	5220
1070	aagccaaaaaa	ggcacaaaaac	agatttaaag	tccctttggg	gacaaaagttt	tacagagtga	5280
1072	aagccgtatc	atggaaataag	aaagtataac	ttatggacaa	aattaataca	ttctatgaca	5340
1074	tttttttctg	atttgcctg	cagtgctcat	tcatcactcc	aaaaacagca	ggccatcttt	5400
1076	ttatgcaaaa	gtcagcgtga	caatataactt	cactgggtga	catcggttac	tttttaactg	5460
1078	gcttcatttt	aggaataata	aattcatcag	aatccttggc	tgaattaaaa	tggttttgc	5520
1080	tttttggttt	tttttttac	ccagacaact	ctagaaatgc	ggaccaaact	acttcatttt	5580
1082	ctcaaagggc	ataccttgc	cattgtggct	tatgatgagc	catattaatt	gcctgttaaa	5640
1084	tatacactag	cttgaactta	gatgttaaat	gttatttttta	ccagcatttg	tcctttgtg	5700
1086	aaatcagttat	cagaataactt	gcactcttta	acacatcttt	tataaaaatgt	ataaaattatt	5760
E--> 1088				-19-			
1089	cagaactatt	taaaataaaag	aggagtgtt	ttgcattgt	ataatcattt	tgagtttgc	5820
1091	tcagtagata	ctaaagcaaa	ttgtttcagt	ttttttaaat	gccctttgt	gttcaaaaaa	5880
1093	aaaaaaaggaa	ctgttaattt	attgactgt	ttaagatca	gccataagta	atcagaacatc	5940
1095	ttcaaaagca	ctttcagttg	attggtcate	tgggttctaa	agggaaaggt	ctgtgtact	6000
1097	aaccatttca	aatgcagact	caaaccctcc	caacatctt	atgactctag	aataatcata	6060
1099	ttgatgaaat	cgtaattcat	ggttgagttt	cagaacaaaa	gatattcatt	gcacattaac	6120
1101	catttagagg	tcatttaaat	aacaaaat	tgtattgtaa	aagaactgt	caattttaaa	6180
1103	acaataaaaga	tttgaacctg	taaatgtgt	tgcctttaa	agaaggatac	attttaata	6240
1105	tatttgagtg	attgctggga	agtgtaaaa	tattgttat	tatcatatca	aagaaaaaca	6300
1107	tgttattac	aaaaatgttc	tttaactata	tactatgtaa	cagggtaaac	agtgttatgt	6360
1109	agaatagaat	tgtgtaaact	agatctttag	agaagttgc	attgagcaaa	gttattttaaa	6420
1111	tgagtttagtt	gagttggatg	agaattgttt	gaggttgc	gctagagaaac	aataataaaa	6480
1113	taattctttt	tcagaaaata	tttaatttct	tcataaaaaat	aagttaaata	ttttttttaaa	6540
1115	tatgtatata	taatagtaca	aaatggataa	aacatcatag	tgtatagaaa	actgaatttg	6600
1117	acaagttat	gaataaaatgt	acaaatgtt	tcaaaa			6636
1120	<210>	SEQ ID NO:	4				
1121	<211>	LENGTH:	6518				
1122	<212>	TYPE:	DNA				

RAW SEQUENCE LISTING

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Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

1123 <213> ORGANISM: Unknown
 1125 <220> FEATURE:
 1126 <223> OTHER INFORMATION: mouse Rb1cc1 gene
 1128 <400> SEQUENCE: 4

1129 ccgagtcgac aataacaaac cccacggcgg ccgcgaccca gccctgccaa gctctcagtg 60
 1131 cctcggccgg cggaactcggg tccccgcgg gagccgaggg gccggagcag cggctgcgcc 120
 1133 cgactcccat cttccggggt actcggcggc tgggcggca cggttgtgtc 180
 1135 gggtggcggc gccgcagggg cggttgatag ccgcgcggc ggccaggcgc gcggcagaag 240
 1137 atggtgccga gggccggcgg ctgtgttgc gccgcggcgg gaggaggcgc tgccggttct 300
 1139 ctgagttca ccagtaatgc cactcagtt ccaatataa gcaagcgcataaagacaat 360
 1141 tgtaatctt taagaaaagt agtacttctc ttacagttt ctggcggatc aacactggag 420
 1143 ggtgaggtgt cagcttccag aaagatcatc atgaagttat atgtgtttt ggttaacacc 480
E--> 1145 -20- *some*

1146 ggaaccacgc tgacattga cactgagcta actgtgcaaa ctgtggctga tcttaagcat 540
 1148 gccattcaaa gcaaatacaa gattgttatt cagcaccagg ttctgggtt caatggagga 600
 1150 gaatgcatgg ctgcagatcg aagagtgtt acttacagcg ctggacggc cacaatcca 660
 1152 attttctt ttaataaaaga aatgatctt tgtgaccgtg cacctgttat tcctaaagct 720
 1154 acctttcaa cagaaaatga catggaaata aaagttgaag agtctttat gatgcgtcga 780
 1156 gtttccaca ctgttgcgtt aaggacacag ctgcagttt aaatgtatga cggtgcgaag 840
 1158 aagctctgtc ctgttgcgtt aaggcttgcgtt catgtatgc acatctcgtc ccaaggctgg 900
 1160 gctgcaatca tggccatct ggaggactgt tcaaattcat accaaaaact tctttcaag 960
 1162 tttgaaaatgtt tttattcttga ttatcttcaa tccatagaag acatcaagtt aaaacttact 1020
 1164 catttagaa ctgtgtttc agtaatggcc aagattccac tattggatgt ccttaaccaga 1080
 1166 catagttaca gggaaatgtt gggaaagaccg gattcttgcgtt atgaacatgtt aggctcag 1140
 1168 aaagctgaga tggaaaatgtt tactgaactg gtgctcttc ctgatatgccc tagaacaacg 1200
 1170 aacacatctt tggtaacccatttccatcatttcaatggcgtt atgtatgttcc agatcccacc 1260
 1172 ggtactgaac gtggcaaaatgttacttggaa tcttgcgttcaaa gtactgtcca gcaagaagaa 1320
 1174 gcttcgttgcgtt atgctaaatgtt cactgtatcg ctgttgcgtt atgtttctt gtttagactgg 1380
 1176 ataaatgttca aagatagacc caatgtatgtt gaatcttgcgtt tcagggatgtt ctgttgcgtt 1440
 1178 atgagcaggc ttgacccaaa gattttcaatgttccatcatttgcgtt tagaatgccc tcaacttatt 1500
 1180 gccaaacttgcgtt ataaatgttcaatgttccatcatttgcgtt tagaatgccc tcaacttatt 1560
 1182 ttggaccaga tgattgttgcgtt ctgtatgttgcgtt ctggtaatgtt aacagaaaaga gcttgcgtt 1620
 1184 ggatttttag ctaatcagat gagatgttgcgtt aacttgcgtt atgcgttgcgtt gttacatgtt 1680
 1186 ctgtgtcttgcgtt atgatgttgcgtt aacttgcgtt aacttgcgtt aacttgcgtt gttacatgtt 1740
 1188 gatattaaac agaagtgcac cactgcgttgcgtt aacttgcgtt aacttgcgtt aacttgcgtt 1800
 1190 ctgaagtgttgcgtt gttttttgtt gatgttgcgtt gctgtatgtt atggagaaaaaactgcgtt 1860
 1192 ctgtccgcgttgcgtt gttttttgtt gatgttgcgtt gctgtatgtt atggagaaaaaactgcgtt 1920
 1194 gttcctcaga tggatgttgcgtt agtgttgcgtt gggatgttgcgtt aacttgcgtt aacttgcgtt 1980
 1196 cactacagat gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt aacttgcgtt 2040
 1198 aagtcaaaaaa gggaaatgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2100
 1200 tttaaaggac tggacttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2160
E--> 1202 -21-

1203 tggatgttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2220
 1205 gaagtgcgttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2280
 1207 gatgttgcgttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2340
 1209 attacatgttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2400
 1211 gcttgcgttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2460
 1213 cttccactaaatgttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2520
 1215 ccagatgttgcgttgcgtt gttttttgtt gatgttgcgtt aacttgcgtt aacttgcgtt 2580

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Input Set : A:\3190-070 Sequence Listing.txt

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1217	caacctgttc	accaagcttc	tatagacttg	gattcattag	cagaaagccc	tgagtctgac	2640
1219	tttatgtctg	ctgtgaatga	gtttgtgata	gaagaaaatt	tatcgctcc	aaaccctata	2700
1221	agtgatccac	aaagtccaga	aatgatggtg	gagtcacttt	actcttcagt	catcaatgca	2760
1223	atagatagta	ggcgtatgca	agacacaagt	acacgtggaa	acgaggggctt	tggggatcg	2820
1225	gctgctctac	atgtccagct	ggagaaatgc	agagctgctg	cacaagactc	tcacaccagt	2880
1227	atacaaacc	tcaaggacga	tctgtccat	ttcagaacat	ttgtacaaaa	agaacagtgt	2940
1229	gacttagcaa	attattttaa	atgtacagct	gtagaaataa	gaaatattat	tgaaaaagta	3000
1231	aaatgttctc	tagaaataac	actaaaggaa	aagcatcagc	aagaactcca	atctttaaaa	3060
1233	attgagttat	aatgtaaact	tgatgctcta	gtaaaaagaca	gtgaagaaaa	tgtaaataaa	3120
1235	attttaaaat	tgaaagaaaa	tttagtatcc	cttgaagagg	cttacaaaa	taaagacaat	3180
1237	gaattcactt	cgattaaaca	tgaaaaggat	gctattgtct	gtgtcagca	agaaaaggat	3240
1239	cagaagttgt	tagagatgga	aaagataatg	catactcaac	attgtgaaat	taaagaactg	3300
1241	aagcagtccac	gagagatggc	attagaagac	ctgaaaaagc	tgcatgatga	aaaaatcgag	3360
1243	tcattgagag	ctgaatttca	gtgcttagaa	gaaaatcacc	tgaaggaatt	agaggacaca	3420
1245	ctgcacatca	ggcacacaca	ggagtttgag	aaagttatga	cagaccacaa	tatgtctttg	3480
1247	gagaaattaa	aaaaagaaaa	ttagcaaaaga	attgaccaga	tgctagaatc	tcatgcctca	3540
1249	actattcagg	aaaagagca	acagctgcag	gagttgaaac	tcaaagttc	tgacttgtca	3600
1251	gacatgagat	gtaagttaga	ggttgaactt	gcactaaagg	aagcagaaac	agatgagata	3660
1253	aagatcttgc	tggaaagagag	cagaacacag	cagaaggaaa	tgctgaagtc	tttacttggaa	3720
1255	caagagaccg	aaaacttaag	aacagaaaata	agtaaactaa	accaaaaaat	tcatgataat	3780
1257	aatgagagtt	accaggtggg	tttgcagag	ttaagagctt	taatgacaat	tgaaaaagat	3840

E--> 1259

-22-

some

1260	cagtgcattt	cagagttat	cagttagacat	gaagaagaat	ctaataact	taaggctgaa	3900
1262	ttagacaatg	ttacatctt	gcatgccaa	gcatatgaaa	tagaaaaaaa	actgaaagaa	3960
1264	caaataatgtt	aattgcagac	tagattgaac	tcagaattga	gtgctttga	aaaacagaaa	4020
1266	gatgaaaaaa	ttacccaaca	agaagagaag	tatgaagcac	ttatccagaa	ccttgagaaa	4080
1268	gacaaggaga	gactggcaa	gaaccacgag	caagacaaag	aacacttaat	tcaggagctt	4140
1270	aattttgaaa	aaaacaaaagc	tgttcaaact	gcactagatg	aatttaaggt	ggagagagaa	4200
1272	cttgcggaaa	aagagttatt	agaaaaagg	aaacatctt	agaatcaa	agccaaaact	4260
1274	cctgccttt	agtcaagccag	agaagattt	tcaagcttag	ttgcggaaact	tcaagagaaa	4320
1276	cttcaagaag	aaaagctaa	gtttctggaa	caacttgaag	aacaagagaa	aagaaagaat	4380
1278	gaggaaatgc	aaaatgtcg	aaccttctt	attgtcgac	agcagaccaa	ctttaacaca	4440
1280	gtcttaacaa	gagagaaaat	gaggaaagaa	aacataataa	atgtatctt	tgataagcta	4500
1282	aaaagtacaa	tgcagcagca	agagcgggat	aaagattga	tagagtgc	ctctgaggac	4560
1284	cgagctcg	tgcttgcaga	gaagaagcag	cttgaagagg	aagtgagtaa	actccgcact	4620
1286	acagtttc	tttcctcagc	acctgtggc	gcagccccag	agctctatgg	tgcgtgtca	4680
1288	cctgagctcc	caggggagcc	agagagatca	gtcatggaga	cggcagatga	aggaagactg	4740
1290	gattccgcaa	tggagacaag	catgtatgt	gtccaaagaaa	acatgttata	tgaagagaag	4800
1292	cagaggatca	tgctctaga	acggacattt	cagttgaaag	aagaagaaaa	caagcggtt	4860
1294	aatcaaagac	tgtatgtca	gagttgtcc	tcagtcctt	caaggcattc	tgaaaaata	4920
1296	gccatttagag	attttcagg	gggagattt	gttctcatca	tccttagatga	gcggcacgac	4980
1298	aattatgtat	tgtttactgt	tagtcctact	ttatattttc	tgcactcaga	gtctttcct	5040
1300	gccctggatc	tcaaaccagg	tgagggagct	tcaggtgc	ctagaagacc	ctgggtcctt	5100
1302	ggaaaagtaa	tggaaaagga	atactgtcaa	gccaaaaagg	cacaaaacag	atttaaagtt	5160
1304	ccttgggaa	caaagtta	cagagtggaa	gctgtgtcat	ggaataagaa	agtatagcca	5220
1306	cagaagaaat	ctctacatct	cataccattt	ttgatttgc	ctccagtgt	gataaaactac	5280
1308	tctaaaaaca	gctggccatt	gttgggtttt	tttttgtt	ttgtttgtt	gtttgtttt	5340
1310	acaaaaagtca	acataacaat	atacttcatt	ggtggactgc	acttacctt	taagtggcta	5400
1312	catcttagga	acaataaatt	tattaaaatt	cttggctgaa	tcaaaatgg	tttggttt	5460

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

1314 ttccacccaa ataactagaa attcggacca aaatagatgt tttccaaggg cagagcctgc 5520
E--> 1316 -23- *yr 24-25 also appear (but not shown on this page)*
 1317 actgtggctt gtgactagcc tcattagttt cctgttaata aacattagct gaatagttac 5580
 1319 cagtgtgtt accagcattt gtccttctgt gaattcaaga gtcctcgac tctttaacat 5640
 1321 gttctttata aaatgtataa acccttccaa actattaaa gaggagtgtt attgcgtca 5700
 1323 gataatcata atttttagtt tgcctcagaa gactactaaa gcaaatttgc tcatttttt 5760
 1325 ttaaaaaaaat gcccttaat gttcaaaaaa aaaataacag tgaatttga ctgactttaa 5820
 1327 gatcagccat aaataatgag cagtcttcaa aagcactttt cacacagatc atctgggctc 5880
 1329 cagggaggaa gagtcgtgc cactgatgtt ttcaagtgc gggactcactc aaacctctca 5940
 1331 gcatcttagg actgtttcaa gtaatcatat tcatgtactc gtaattcatg gttgaccttc 6000
 1333 agaagaagat attcattgtt tattaaacatt tagaggtcat taaaataaca aaagtctgt 6060
 1335 ttgtaaagga cctgtacaat ttaagacaaa taaagaattt aaagtgtaaa tttgtgtgcc 6120
 1337 ttttaaaggat tacattttaa atatattgcg tgatttctgg gaaaggtgaa aaaaatgttc 6180
 1339 tttatcaaaag agaaacctgt ttattaaaaa atgttgcattt tttcctatgt aacagggtga 6240
 1341 agtgggttgc tttggaaacag aaccatgtttt actcaagggtt taaaagctgg cactgtacaa 6300
 1343 agatattgaa gtatcttaggc tagttgattt gaaagagttt cttcagggtt gttgttagca 6360
 1345 gtaataaaatg attcttttc agaaatattt aatttctcca taaaataaaatg ttggatattt 6420
 1347 ttataaaatg gtaatctaat agaatgaaaaa tggataaaac atagtgtata gaatacctaa 6480
 1349 ttcaaaaaaca tattatgaa taaacgaaca aatgatta 6518
 1475 <210> SEQ ID NO: 15
 1476 <211> LENGTH: 21
 1477 <212> TYPE: DNA
 1478 <213> ORGANISM: Artificial
 1480 <220> FEATURE:
 1481 <223> OTHER INFORMATION: artificially synthesized primer sequence called

CC1-S8

1483 <400> SEQUENCE: 15
 1484 aaggaagacc tttgccactt t

21

-26-

*also yr 29-30***E--> 1487**

1645 <210> SEQ ID NO: 29
 1646 <211> LENGTH: 20
 1647 <212> TYPE: DNA
 1648 <213> ORGANISM: Artificial
 1650 <220> FEATURE:

1651 <223> OTHER INFORMATION: artificially synthesized primer sequence called
RB1CC-R3

1653 <400> SEQUENCE: 29
 1654 aaactcagaa aaccggcaac

20

-29-

*also 30-31***E--> 1657**

1818 <210> SEQ ID NO: 43
 1819 <211> LENGTH: 20
 1820 <212> TYPE: DNA
 1821 <213> ORGANISM: Artificial
 1823 <220> FEATURE:

1824 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MMK1-2-S

1826 <400> SEQUENCE: 43
 1827 taagcatgcc attcaaagca

20

-32-

E--> 1830

1990 <210> SEQ ID NO: 57
 1991 <211> LENGTH: 20
 1992 <212> TYPE: DNA

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006
TIME: 12:25:14

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

1993 <213> ORGANISM: Artificial
1995 <220> FEATURE:
1996 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MCC-S8
1998 <400> SEQUENCE: 57
1999 acgtggcaaa gaacttaggg
E--> 2003
2161 <210> SEQ ID NO: 71
2162 <211> LENGTH: 20
2163 <212> TYPE: DNA
2164 <213> ORGANISM: Artificial
2166 <220> FEATURE:
2167 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MCC-AS3
2169 <400> SEQUENCE: 71
2170 tgccgctcat ctaggatgat
E--> 2174
2394 <210> SEQ ID NO: 90
2395 <211> LENGTH: 20
2396 <212> TYPE: DNA
2397 <213> ORGANISM: Artificial
2399 <220> FEATURE:
2400 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MINT2-S0
2402 <400> SEQUENCE: 90
2403 tgccactcag ttgccaagta
E--> 2404
2564 <210> SEQ ID NO: 104
2565 <211> LENGTH: 20
2566 <212> TYPE: DNA
2567 <213> ORGANISM: Artificial
2569 <220> FEATURE:
2570 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MINT9-AS
2572 <400> SEQUENCE: 104
2573 gcctgcagtt tttctccatc
E--> 2576
2738 <210> SEQ ID NO: 118
2739 <211> LENGTH: 20
2740 <212> TYPE: DNA
2741 <213> ORGANISM: Artificial
2743 <220> FEATURE:
2744 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MINT16-AS
2746 <400> SEQUENCE: 118
2747 gctcttgctg ctgcattgt
E--> 2751
2910 <210> SEQ ID NO: 132
2911 <211> LENGTH: 20
2912 <212> TYPE: DNA
2913 <213> ORGANISM: Artificial
2915 <220> FEATURE:
2916 <223> OTHER INFORMATION: artificially synthesized primer sequence called

-35-

also 33-34

20

-38-

also 36-37

20

-42-

also 39-41

20

-45-

also 42-44

20

primer

-48-

also 45-47

20

Sequence

sequence

MINT23-AS
2918 <400> SEQUENCE: 132

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:14

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

2919 cagcactgga ggacaaatca
E--> 2922

20

-51-

also 49-50

19
VERIFICATION SUMMARY
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006
TIME: 12:25:15

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:515 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:915 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=3
L:1145 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=4
L:1374 M:283 W: Missing Blank Line separator, <400> field identifier
L:1430 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:1487 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:1545 M:283 W: Missing Blank Line separator, <400> field identifier
L:1601 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:1602 M:283 W: Missing Blank Line separator, <220> field identifier
L:1657 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:1717 M:283 W: Missing Blank Line separator, <400> field identifier
L:1773 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:1774 M:283 W: Missing Blank Line separator, <220> field identifier
L:1830 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:1888 M:283 W: Missing Blank Line separator, <400> field identifier
L:1945 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2003 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2061 M:283 W: Missing Blank Line separator, <400> field identifier
L:2117 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2118 M:283 W: Missing Blank Line separator, <220> field identifier
L:2174 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2232 M:283 W: Missing Blank Line separator, <400> field identifier
L:2290 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2291 M:283 W: Missing Blank Line separator, <220> field identifier
L:2347 M:259 W: Allowed number of lines exceeded, <211> LENGTH:
L:2404 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2518 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2519 M:283 W: Missing Blank Line separator, <220> field identifier
L:2576 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2638 M:283 W: Missing Blank Line separator, <400> field identifier
L:2694 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2695 M:283 W: Missing Blank Line separator, <220> field identifier
L:2751 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2809 M:283 W: Missing Blank Line separator, <400> field identifier
L:2865 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2866 M:283 W: Missing Blank Line separator, <220> field identifier
L:2922 M:254 E: No. of Bases conflict, this line has no nucleotides.